IN THE CLAIMS

Please amend the claims as follows:

Claim 1 (Currently Amended) A system for determining the level of a biological indicator within a patient sample applied to an array, where <u>material associated with</u> the array includes emitters emitting data indicative of the biological indicator, based on digitized output patterns from the array, comprising:

a preconditioning unit <u>that</u> for pre-condition<u>s</u>ing the digitized output pattern <u>to facilitate an interferometric interaction</u>;

an interferometric unit configured to generate an interference between the pre-conditioned digitized output pattern and a reference wave to enhance the digitized output pattern; and

an analysis unit for analyzing the interferometrically enhanced digitized output pattern to determine the level of the biological indicator.

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Claim 2 (Currently Amended) A system for determining the level of specific constituents within an output pattern generated from a detected image of a biological sample applied to an array wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, comprising:

tessellation means for tessellating the output pattern to facilitate an interferometric interaction;

signal processing means for amplifying signals associated with the biological sample within the tessellated output pattern, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

first determination means for determining which signals within the modified output pattern correlate with specific constituents within the biological sample; second determination means for determining specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

third determination means for associating the signals correlating to specific constituents with levels of such specific constituents within the sample.

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Claim 3 (Currently Amended)   A system for quantitating specific constituents within an output pattern generated from a detected image of a biological sample applied to an array wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, comprising:

a tessellation unit for segmenting the output pattern;

a signal processing unit to amplify signals associated with the biological sample within the segmented output pattern, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

a first determination unit to determine which signals within the modified output pattern correlate with specific constituents within the biological sample;

a second determination unit to determine specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

a mapping unit to for mapping the signals correlating to specific constituents on a diffusion curve to determine the level of such specific constituents within the biological sample.

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Claim 4 (Original) A technique for analyzing an output pattern of a biological sample applied to an array to determine the presence and quantity of specific constituents within a biological sample applied to the array, wherein the output pattern comprises signals associated with noise, and signals correlating to the biological sample with the signals correlating to the biological sample having intensities both greater and less than the signals associated with noise, the method comprising the steps of:

segmenting the output pattern of the array using tessellation;

interferometrically enhancing the segmented output pattern to amplify signals associated with the biological sample, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

associating signals within the interferometrically enhanced segmented output pattern with specific constituents within the biological sample; and

determining specific constituents within the biological sample based on the signals within the interferometrically enhanced segmented output pattern associated with specific constituents within the biological sample; and

mapping the signals associated with specific constituents to a diffusion curve.

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Claim 5 (Currently Amended) A computer code product, <u>embodied on computer readable media</u>, that determines the presence of specific constituents within an output pattern of a biological sample applied to an array of detectors, wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, the computer code product comprising:

computer code that segments the output pattern using tessellation;

computer code that utilizes signal processing to amplify signals within the segmented output pattern associated with the biological sample having an intensity lower than the intensity of the signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

computer code that determines which signals within the modified output pattern correlate with specific constituents within the biological sample; and

computer code that determines specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

computer code that maps signals correlating to specific constituents to a diffusion curve.

Claims 6 – 12 (Canceled)

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Claim 13 (Currently Amended) A method for determining the level of a biological indicator within a patient sample applied to an arrayed information structure, where material associated with the arrayed information structure emits data indicative of the biological indicator, based on digitized output patterns from the arrayed information structure, comprising the steps of:

pre-conditioning the digitized output pattern to facilitate an interferometric interaction;

generating an interference between the pre-conditioned digitized output pattern and a reference wave to enhance the digitized output pattern; and

analyzing the interferometrically enhanced digitized output pattern to determine the level of the biological indicator.

Claim 14 (Currently Amended) The method of claim 13, wherein the analyzing step comprises:

generating a diffusion curve with a biological indicator of interest;

mapping the output patterns to the diffusion curve; and

determining the degree of convergence between the mapped coordinates of the respective output patterns mapped on the diffusion curve.

Claim 15 (Previously Presented) The method of claim 14 further comprising the step of interferometrically enhancing the output patterns prior to the mapping step.

Claim 16 (Previously Presented) The method of claim 15 wherein the interferometric enhancement step utilizes at least one of the group comprising: resonance interferometry, quantum resonance interferometry, and stochastic resonance interferometry.

Claim 17 (Previously Presented) The method of claim 15 further comprising the step of tessellating the output pattern prior to the interferometric enhancement step.

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Claim 18 (Previously Presented) The method of claim 14 further comprising the step of performing nucleic acid amplification to enhance the output patterns prior to the mapping step.

Claim 19 (Previously Presented) The method of claim 14 wherein the sample is selected from a group consisting of DNA, RNA, protein, peptide-nucleic acid (PNA) and targeted nucleic acid (TNA) samples.

Claim 20 (Previously Presented) The method of claim 13 further comprising the step of tessellating the enhanced output pattern prior to the analyzing step.

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